

**Amendments to the Specification:**

Please replace the paragraph beginning at page 10, lines 7-15, with the following rewritten paragraph:

**FIGURE 14.** Potential functional domains of TARP (SEQ ID NO: 14). (A) TARP contains a potential leucine zipper motif and phosphorylation sites. A potential leucine zipper motif is indicated with boxed leucines followed by a basic region that is underlined. cAMP- and cGMP-dependent protein kinase phosphorylation sites (amino acids 46-49 and 55-58, see SEQ ID NO: 14) and protein kinase C phosphorylation sites (amino acids 19-21 and 20-22, see SEQ ID NO: 15) are outlined. (B) Protein sequence comparison of TARP with Tup1. Amino acids sequences for TARP (42-57, SEQ ID NO: 16), *Dictyostelium discoideum* Tup1 (dTup1, 521-536, SEQ ID NO: 17) and *Saccharomyces cerevisiae* Tup1 (yTup1, 626-660, SEQ ID NO: 18) are shown. Conserved residues are boxed.